

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Yu, Lei
- (ii) TITLE OF INVENTION: Mu Opioid Receptors:
Compositions and Methods
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold, White & Durkee
 - (B) STREET: 321 North Clark Street, Suite 800
 - (C) CITY: Chicago
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 60610
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Northrup, Thomas E.
 - (B) REGISTRATION NUMBER: 33,268
 - (C) REFERENCE/DOCKET NUMBER: ARCD095
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312-744-0090
 - (B) TELEFAX: 312-755-4489

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (cdna)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 214..1410
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGTGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG	60
CCGCTCTTCT CTGGTTCCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA	120
GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC	180
AGCCTACCTA GTCCGCAGCA GGCCTTCAGC ACC ATG GAC AGC AGC ACC GGC CCA	234
Met Asp Ser Ser Thr Gly Pro	
5	

CGG ATG GTG CTG GTG GTC GTG GCT GTA TTT ATC GTC TGC TGG ACC CCC	1098
Arg Met Val Leu Val Val Val Ala Val Phe Ile Val Cys Trp Thr Pro	
280 285 290 295	
ATC CAC ATC TAC GTC ATC ATC AAA GCG CTG ATC ACG ATT CCA GAA ACC	1146
Ile His Ile Tyr Val Ile Ile Lys Ala Leu Ile Thr Ile Pro Glu Thr	
300 305 310	
ACA TTT CAG ACC GTT TCC TGG CAC TTC TGC ATT GCT TTG GGT TAC ACG	1194
Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala Leu Gly Tyr Thr	
315 320 325	
AAC AGC TGC CTG AAT CCA GTT CTT TAC GCC TTC CTG GAT GAA AAC TTC	1242
Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe	
330 335 340	
AAG CGA TGC TTC AGA GAG TTC TGC ATC CCA ACC TCG TCC ACG ATC GAA	1290
Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Thr Ile Glu	
345 350 355	
CAG CAA AAC TCC ACT CGA GTC CGT CAG AAC ACT AGG GAA CAT CCC TCC	1338
Gln Gln Asn Ser Thr Arg Val Arg Gln Asn Thr Arg Glu His Pro Ser	
360 365 370 375	
ACG GCT AAT ACA GTG GAT CGA ACT AAC CAC CAG CTA GAA AAT CTG GAG	1386
Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Leu Glu Asn Leu Glu	
380 385 390	
GCA GAA ACT GCT CCA TTG CCC TAACTGGGTC TCACACCATC CAGACCCTCG	1437
Ala Glu Thr Ala Pro Leu Pro	
395	
CTAAGCTTAG AGGCCGCCAT CTACG1GGAA TCAGGTTGCT GTCAGGGTGT GTGGGAGGCT	1497
CTGGTTTCCT GAGAAACCAT CTGATCCTGC ATTCAAAGTC ATTCCTCTCT GGCTACTTCA	1557
CTCTGCACAT GAGAGATGCT CAGACTGATC AAGACCAGAA GAAAGAAGAG ACTACCGGAC	1617
A	1618

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Ser Ser Thr Gly Pro Gly Asn Thr Ser Asp Cys Ser Asp Pro	
1 5 10 15	
Leu Ala Gln Ala Ser Cys Ser Pro Ala Pro Gly Ser Trp Leu Asn Leu	
20 25 30	
Ser His Val Asp Gly Asn Gln Ser Asp Pro Cys Gly Leu Asn Arg Thr	
35 40 45	
Gly Leu Gly Gly Asn Asp Ser Leu Cys Pro Gln Thr Gly Ser Pro Ser	
50 55 60	
Met Val Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val Cys Val	
65 70 75 80	

Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val Arg Tyr
85 90 95

Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu
100 105 110

Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Asn Tyr
115 120 125

Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile Val Ile
130 135 140

Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Cys Thr
145 150 155 160

Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu
165 170 175

Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Val Asn Val Cys Asn Trp
180 185 190

Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala Thr Thr
195 200 205

Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Pro
210 215 220

Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile Phe Ala
225 230 235 240

Phe Ile Met Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Ile
245 250 255

Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp
260 265 270

Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val Ala Val
275 280 285

Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala
290 295 300

Leu Ile Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe
305 310 315 320

Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val Leu Tyr
325 330 335

Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe Cys Ile
340 345 350

Pro Thr Ser Ser Thr Ile Glu Gln Gln Asn Ser Thr Arg Val Arg Gln
355 360 365

Asn Thr Arg Glu His Pro Ser Thr Ala Asn Thr Val Asp Arg Thr Asn
370 375 380

His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1618 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 339..1235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGTGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG	60
CCGCTCTTCT CTGGTTCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA	120
GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC	180
AGCCTACCTA GTCCGCAGCA GGCCTTCAGC ACCATGGACA GCAGACCCGG CCCAGGGAAC	240
ACCAGCGACT GCTCAGACCC CTTAGCTCAG GCAAGTTGCT CCCCAGCACC TGGCTCCTGG	300
CTCAACTTGT CCCACGTTGA TGGCAACCAG TCCGATCC ATG CGG TCT GAA CCG	353
Met Arg Ser Glu Pro	
1 5	
CAC CGG GCT TGG CGG GAA CGA CAG CCT GTG CCC TCA GAC CGG CAG CCC	401
His Arg Ala Trp Arg Glu Arg Gln Pro Val Pro Ser Asp Arg Gln Pro	
10 15 20	
TTC CAT GGT CAC AGC CAT TAC CAT CAT GGC CCT CTA CTC TAT CGT GTG	449
Phe His Gly His Ser His Tyr His His Gly Pro Leu Leu Tyr Arg Val	
25 30 35	
TGT AGT GGG CCT CTT CGG AAA CTT CCT GGT CAT GTA TGT GAT TGT AAG	497
Cys Ser Gly Pro Leu Arg Lys Leu Pro Gly His Val Cys Asp Cys Lys	
40 45 50	
ATA CAC CAA AAT GAA GAC TGC CAC CAA CAT CTA CAT TTT CAA CCT TGC	545
Ile His Gln Asn Glu Asp Cys His Gln His Leu His Phe Gln Pro Cys	
55 60 65	
TCT GGC AGA CGC CTT AGC GAC CAG TAC ACT GCC CTT TCA GAG TGT CAA	593
Ser Gly Arg Arg Leu Ser Asp Gln Tyr Thr Ala Leu Ser Glu Cys Gln	
70 75 80 85	
CTA CCT GAT GGG AAC ATG GCC CTT CGG AAC CAT CCT CTG CAA GAT CGT	641
Leu Pro Asp Gly Asn Met Ala Leu Arg Asn His Pro Leu Gln Asp Arg	
90 95 100	
GAT CTC AAT AGA TTA CTA CAA CAT GTT CAC CAG CAT ATT CAC CCT CTG	689
Asp Leu Asn Arg Leu Leu Gln His Val His Gln His Ile His Pro Leu	
105 110 115	
CAC CAT GAG CGT GGA CCG CTA CAT TGC TGT CTG CCA CCC AGT CAA AGC	737
His His Glu Arg Gly Pro Leu His Cys Cys Leu Pro Pro Ser Gln Ser	
120 125 130	
CCT GGA TTT CCG TAC CCC CCG AAA TGC CAA AAT CGT CAA CGT CTG CAA	785
Pro Gly Phe Pro Tyr Pro Pro Lys Cys Gln Asn Arg Gln Arg Leu Gln	
135 140 145	

CTG GAT CCT CTC TTC TGC CAT CGG TCT GCC TGT AAT GTT CAT GGC AAC	833
Leu Asp Pro Leu Phe Cys His Arg Ser Ala Cys Asn Val His Gly Asn	
150 155 160 165	
CAC AAA ATA CAG GCA GGG GTC CAT AGA TTG CAC CCT CAC GTT CTC CCA	881
His Lys Ile Gln Ala Gly Val His Arg Leu His Pro His Val Leu Pro	
170 175 180	
CCC AAC CTG GTA CTG GGA GAA CCT GCT CAA AAT CTG TGT CTT TAT CTT	929
Pro Asn Leu Val Leu Gly Glu Pro Ala Gln Asn Leu Cys Leu Tyr Leu	
185 190 195	
CGC TTT CAT CAT GCC GAT CCT CAT CAT CAC TGT GTG TTA CGG CCT GAT	977
Arg Phe His His Ala Asp Pro His His His Cys Val Leu Arg Pro Asp	
200 205 210	
GAT CTT ACG ACT CAA GAG CGT TCG CAT GCT ATC GGG CTC CAA AGA AAA	1025
Asp Leu Thr Thr Gln Glu Arg Ser His Ala Ile Gly Leu Gln Arg Lys	
215 220 225	
GGA CAG GAA TCT GCG CAG GAT CAC CCG GAT GGT GCT GGT GGT CGT GGC	1073
Gly Gln Glu Ser Ala Gln Asp His Pro Asp Gly Ala Gly Gly Arg Gly	
230 235 240 245	
TGT ATT TAT CGT CTG CTG GAC CCC CAT CCA CAT CTA CGT CAT CAT CAA	1121
Cys Ile Tyr Arg Leu Asp Pro His Pro His Leu Arg His His Gln	
250 255 260	
AGC GCT GAT CAC GAT TCC AGA AAC CAC ATT TCA GAC CGT TTC CTG GCA	1169
Ser Ala Asp His Asp Ser Arg Asn His Ile Ser Asp Arg Phe Leu Ala	
265 270 275	
CTT CTG CAT TGC TTT GGG TTA CAC GAA CAG CTG CCT GAA TCC AGT TCT	1217
Leu Leu His Cys Phe Gly Leu His Glu Gln Leu Pro Glu Ser Ser Ser	
280 285 290	
TTA CGC CTT CCT GGA TGAAACTTC AAGCGATGCT TCAGAGAGTT CTGCATCCCA	1272
Leu Arg Leu Pro Gly	
295	
ACCTCGTCCA CGATCGAACA GCAAACTCC ACTCGAGTCC GTCAGAACAC TAGGGAACAT	1332
CCCTCCACGG CTAATACAGT GGATCGAACT AACCACCAGC TAGAAAATCT GGAGGCAGAA	1392
ACTGCTCCAT TGCCCTAACT GGGTCTCACA CCATCCAGAC CCTCGCTAAG CTTAGAGGCC	1452
GCCATCTACG TGAATCAGG TTGCTGTCAG GGTGTGTGGG AGGCTCTGGT TTCCTGAGAA	1512
ACCATCTGAT CCTGCATTCA AAGTCATTCC TCTCTGGCTA CTTCACTCTG CACATGAGAG	1572
ATGCTCAGAC TGATCAAGAC CAGAAGAAAG AAGAGACTAC CGGACA	1618

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Ser Glu Pro His Arg Ala Trp Arg Glu Arg Gln Pro Val Pro
1 5 10 15

Ser Asp Arg Gln Pro Phe His Gly His Ser His Tyr His His Gly Pro
20 25 30

Leu Leu Tyr Arg Val Cys Ser Gly Pro Leu Arg Lys Leu Pro Gly His
35 40 45

Val Cys Asp Cys Lys Ile His Gln Asn Glu Asp Cys His Gln His Leu
50 55 60

His Phe Gln Pro Cys Ser Gly Arg Arg Leu Ser Asp Gln Tyr Thr Ala
65 70 75 80

Leu Ser Glu Cys Gln Leu Pro Asp Gly Asn Met Ala Leu Arg Asn His
85 90 95

Pro Leu Gln Asp Arg Asp Leu Asn Arg Leu Leu Gln His Val His Gln
100 105 110

His Ile His Pro Leu His His Glu Arg Gly Pro Leu His Cys Cys Leu
115 120 125

Pro Pro Ser Gln Ser Pro Gly Phe Pro Tyr Pro Pro Lys Cys Gln Asn
130 135 140

Arg Gln Arg Leu Gln Leu Asp Pro Leu Phe Cys His Arg Ser Ala Cys
145 150 155 160

Asn Val His Gly Asn His Lys Ile Gln Ala Gly Val His Arg Leu His
165 170 175

Pro His Val Leu Pro Pro Asn Leu Val Leu Gly Glu Pro Ala Gln Asn
180 185 190

Leu Cys Leu Tyr Leu Arg Phe His His Ala Asp Pro His His His Cys
195 200 205

Val Leu Arg Pro Asp Asp Leu Thr Thr Gln Glu Arg Ser His Ala Ile
210 215 220

Gly Leu Gln Arg Lys Gly Gln Glu Ser Ala Gln Asp His Pro Asp Gly
225 230 235 240

Ala Gly Gly Arg Gly Cys Ile Tyr Arg Leu Leu Asp Pro His Pro His
245 250 255

Leu Arg His His Gln Ser Ala Asp His Asp Ser Arg Asn His Ile Ser
260 265 270

Asp Arg Phe Leu Ala Leu Leu His Cys Phe Gly Leu His Glu Gln Leu
275 280 285

Pro Glu Ser Ser Ser Leu Arg Leu Pro Gly
290 295

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATCTTCACCC TCACCATGAT G

21

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGTCCTTCT CCTTGAACC

20